

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Method of screening modified antibody having agonistic activity

<130> C1-A0322P

<150> JP 2003-415733

<151> 2003-12-12

<160> 15

<170> PatentIn version 3.1

<210> 1

<211> 21

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 1

gggccagtgg atagacagat g

21

<210> 2

<211> 23

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 2

gctcactgga tgggtggaag atg

23

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 <211> 411
 <212> DNA
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<220>
 <221> CDS
 <222> (1)..(411)
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 Met Glu Trp Pro Leu Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15
 gtc cac tcc cag gtt cag ctg cag cag tct gga cct gag ttg gtg aag 96
 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 cct ggg gcc tca gtg aag att tcc tgc aag gct tct ggc tat gca ttc 144
 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
 35 40 45
 agt agt tcc tgg atg aac tgg gtg aag cag agg cct gga aag ggt ctt 192
 Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu
 50 55 60
 gag tgg att gga cgg att tat cct gga gat gga gat act aac tac aat 240
 Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn
 65 70 75 80
 ggg aag ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc 288
 Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

acg gcc tac ata caa ctc agc agc cta aca tct gag gac tct gcg gtc 336
Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

tac ttc tgt gca aga ggg tat gct gac tac tcc ttt gct tac tgg ggc 384
 Tyr Phe Cys Ala Arg Gly Tyr Ala Asp Tyr Ser Phe Ala Tyr Trp Gly
 115 120 125

caa ggg act ctg gtc act gtc tct gca 411
Gln Gly Thr Leu Val Thr Val Ser Ala
130 135

<210>	4
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<212>	PRT
<213>	Mus musculus

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Met Glu Trp Pro Leu Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
35 40 45

Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn
65 70 75 80

Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Phe Cys Ala Arg Gly Tyr Ala Asp Tyr Ser Phe Ala Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ala
130 135

<210> 5

<211> 396

<212> DNA

<213> Mus musculus

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<221> CDS

<222> (1).. (396)

<223>

<400> 5

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Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15

gga gcc att ggg gat att gtg atg act cag gct gca ccc tct gta cct 96
Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro
20 25 30

gtc act cct gga gag tca gta tcc atc tcc tgc agg tct agt aag agt 144
Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45

ctc ctg cat agt aat ggc aac act tac ttg tat tgg ttc ctg cag agg 192
Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg
50 55 60

cca ggc cag tct cct cag ctc ctg ata tat cgg atg tcc aac ctt gcc 240
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala
 65 70 75 80

tca gga gtc cca gac agg ttc agt ggc agt ggg tca gga act gct ttc 288
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe
 85 90 95

aca ctg aga atc agt aga gtg gag gct gag gat gtg ggt gtt tat tac 336
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 105 110

tgt atg caa cat cta gaa tat ccg tat acg ttc gga tcg ggg acc aag 384
 Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Ser Gly Thr Lys
 115 120 125

ctg gaa ata aaa 396
 Leu Glu Ile Lys
 130

<210> 6
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 <212> PRT
 <213> Mus musculus

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Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro
 20 25 30

Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser
 35 40 45

Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg

50	55	60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala		
65	70	75 80
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe		
	85	90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr		
	100	105 110
Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Ser Gly Thr Lys		
	115	120 125
Leu Glu Ile Lys		
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<210> 7

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<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

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tagaattcca ccatggaatg gcctttgatc

30

<210> 8

<211> 56

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 8

agcctgagtc atcacaatat ccgatccgcc tccacctgca gagacagtga ccagag 56

<210> 9

<211> 56

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 9

actctggtca ctgtctctgc aggtggaggc ggatcggata ttgtgatgac tcaggc 56

<210> 10

<211> 60

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 10

attgcggccg cttatcactt atcgtcgtca tccttgtagt cttttatttc cagcttggtc 60

<210> 11

<211> 8

<212> PRT

<213> Artificial

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<223> an artificially synthesized FLAG tag sequence

<400> 11

Asp Tyr Lys Asp Asp Asp Asp Lys

<210> 12

<211> 82

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 12

tgagtcatca caatatccga tccgccacca cccgaaccac caccacccga accaccacca 60

cctgcagaga cagtgaccag ag 82

<210> 13

<211> 82

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 13

tggtcactgt ctctgcaggt ggtggtggtt cgggtggtgg tggttcgggt ggtggcggat 60

cggatattgt gatgactcag gc 82

<210> 14

<211> 25

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 14

caggttcagc tgcagcagtc tggac

25

<210> 15

<211> 81

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 15

gctgcagctg aacctgcgat ccaccgcctc ccgaaccacc accaccgat ccaccacctc 60

cttttatttc cagcttggtc c 81